What is Claimed is:

1. A method of detecting metastatic melanoma cells in a patient comprising:

(a) isolating nucleic acid from a biological sample obtained from the patient;

(b) amplifying nucleic acid targets, if present, from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both; and

(c) detecting the presence or absence of the nucleic acid targets.

2. The method of claim 1 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, MART-1, MITF, TRP-2, and Tyrosinase.

3. The method of claim 1 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; a second combination of MART-1, GalNAcT, MITF, and PAX3; a third combination of MART-1, TRP-2, GalNAcT, and PAX3; or a fourth combination of Tyrosinase, MART-1, GalNAcT, and PAX3.

4. The method of claim 1 wherein the nucleic acid is mRNA and the nucleic acid targets are amplified using real-time reverse transcriptase polymerase chain reaction (qRT-PCR).

5. The method of claim 1 wherein the biological sample is selected from a group consisting of paraffin-embedded (PE) melanoma tissues, frozen lymph nodes, and PE lymph nodes.

6. The method of claim 1, wherein the biological sample is histopathologically negative for melanoma cells.

7. The method of claim 6, wherein histopathology of the biological sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8. The method of claim 1 further comprising a step of assigning an AJCC (American Joint Committee on Cancer) stage to the patient based on the presence or absence of the nucleic acid targets in the sample.

9. The method of claim 1 further comprising a step of predicting at least one parameter selected from a group consisting of disease recurrence, patient's prognosis, and patient's survival, wherein the parameters is determined based on the presence or absence of the nucleic acid targets in the sample.

10. The method of claim 9, wherein the parameter is predicted for at least three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11. The method of claim 9 further comprising a step of selecting a treatment regimen based on the patient's prognosis.

12. A method of detecting metastatic melanoma cells in a patient comprising:

(a) preparing PE samples from tissues or lymph nodes of the patient;

(b) deparaffinizing the PE samples to obtain deparaffinized samples;

(c) isolating nucleic acid from the deparaffinized samples;

(d) amplifying nucleic acid targets, if present, from a panel of marker genes, wherein the panel comprises at least two marker genes selected from a group consisting of MAGE-A3, GalNAcT, MART-1, PAX3, MITF, TRP-2, and Tyrosinase; and

(e) detecting the presence or absence of the nucleic acid targets.

13. The method of claim 12 wherein the nucleic acid is mRNA and the nucleic acid targets are amplified using qRT-PCR.

14. A method of detecting metastatic breast, gastric, pancreas or colon cancer cells in a patient comprising:

(a) isolating nucleic acid from PE cancerous tissues or PE lymph nodes of the patient;

(b) amplifying nucleic acid targets, if present, from a panel of marker genes selected from a group consisting of C-Met, MAGE-A3, Stanniocalcin-l, mammoglobin, HSP27, GalNAcT, CK20, and β-HCG; and

(c) detecting the presence or absence of the nucleic acid targets.

15. The method of claim 14 wherein the panel comprises a first combination of C-Met, MAGE-A3, GalNAcT, and CK20; a second combination of mammoglobulin, C-Met, GalNAcT, and β-HCG; a third combination of mammoglobulin, β-HCG, HSP27, and C-Met; or a fourth combination of HSP27, CK20, Stanniocalcin-1, and MAGE-A3.

16. The method of claim 14 wherein the nucleic acid is mRNA and the nucleic acid targets are amplified using qRT-PCR.

17. The method of claim 14, wherein the biological sample is histopathologically negative for melanoma cells.

18. The method of claim 17, wherein histopathology of the biological sample is determined by hematoxylin and eosin staining or immunohistochemistry.

19. The method of claim 14 further comprising a step of assigning an AJCC stage to the patient based on the presence or absence of the nucleic acid targets in the sample.

20. The method of claim 14 further comprising a step of predicting at least one parameter selected from a group consisting of disease recurrence, patient's prognosis, and patient's survival, wherein the parameters is determined based on the presence or absence of the nucleic acid targets in the sample.

21. The method of claim 20, wherein the parameter is predicted for at least three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

22. The method of claim 20 further comprising a step of selecting a treatment regimen based on the patient's prognosis.

23. A kit for use in detecting melanoma cells in a biological sample comprising:

(a) primers for amplifying nucleic acids targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both, and

(b) containers for each of the pairs of primers.

24. The kit of claim 23 further comprising primers from marker genes selected from a group consisting of MAGE-A3, MART-1, MITF, TRP-2, and Tyrosinase.

25. The kit of claim 23, further comprising enzymes and reagents for the preparation of cDNAs.

26. The kit of claim 23, further comprising enzymes and reagents for chromophoric labeling of nucleic acids.